



HAL
open science

Draft Genome Sequence of *Collimonas pratensis* Strain PMB3(1), an Effective Mineral-Weathering and Chitin-Hydrolyzing Bacterial Strain

Laura Picard, Phil M. Oger, Marie-Pierre M.-P. Turpault, Stephane Uroz

► **To cite this version:**

Laura Picard, Phil M. Oger, Marie-Pierre M.-P. Turpault, Stephane Uroz. Draft Genome Sequence of *Collimonas pratensis* Strain PMB3(1), an Effective Mineral-Weathering and Chitin-Hydrolyzing Bacterial Strain. *Microbiology Resource Announcements*, 2020, 9 (37), 10.1128/MRA.00601-20 . hal-02939115

HAL Id: hal-02939115

<https://hal.science/hal-02939115v1>

Submitted on 3 Nov 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Draft Genome Sequence of *Collimonas pratensis* Strain PMB3(1), an Effective Mineral-Weathering and Chitin-Hydrolyzing Bacterial Strain

Laura Picard,^{a,b} Philippe Oger,^c Marie-Pierre Turpault,^b Stéphane Uroz^{a,b}

^aUniversité de Lorraine, INRAe, UMR 1136 Interactions Arbres-Microorganismes, Champenoux, France

^bINRAe, UR 1138 Biogéochimie des Écosystèmes Forestiers, Champenoux, France

^cUniversité de Lyon, INSA de Lyon, Université Claude Bernard Lyon 1, CNRS UMR 5240, Lyon, France

ABSTRACT We announce the draft genome sequence of *Collimonas pratensis* PMB3(1), isolated from the *Scleroderma citrinum* mycorrhizosphere. In addition to its mineral-weathering effectiveness and antifungal activity, this strain is characterized by genomic features that give it great potential as a biocontrol and plant growth-promoting agent in nutrient-poor soils.

In temperate regions, forests develop mostly on nutrient-poor and acidic soils, in which minerals represent essential sources of nutritive cations (Ca, Mg, K, Fe). Cations entrapped in these minerals are made bioavailable to the plants through a dissolution process termed “mineral weathering,” in which bacteria play an essential part (1). *Collimonas* species are considered very effective mineral-weathering and plant-growth-promoting bacteria (1, 2). Representatives of this genus belong to the *Oxalobacteraceae* family, which comprises four described species (*C. anthrihumii*, *C. arenae*, *C. fungivorans*, and *C. pratensis*) (3–5). Collimonads are members of the rare biosphere found in acidic soils, with low nutrient availability and often in interaction with fungi (6–9). Strain PMB3(1) was isolated from oak rhizosphere on 10% tryptic soy agar (TSA) medium and cryopreserved in 40% glycerol.

Strain PMB3(1) was grown at 25°C in LB medium to late exponential phase. The cell pellet was lysed with lysozyme (1 mg/ml) at 50°C for 1 h, sodium dodecyl sulfate (final concentration, 1%), and proteinase K (final concentration, 1 mg/ml), followed by chloroform purification and ethanol precipitation as described by Pospiech and Neumann (10). The libraries were prepared using the Kapa HyperPlus kit (Roche) and Nextera XT DNA library preparation kit (Illumina), following the manufacturer’s instructions. A combination of a mate pair library of 3 kb, an unpaired fragment library of 500-bp fragments done on a GS-FLX 454 system (Roche), and an Illumina library of 100-bp reads done on a MiSeq instrument (Beckman Coulter Genomics, Danvers, MA, USA) was effected. A total of 111,000 454 reads and 41 million Illumina reads were generated, providing 309 Mb of 454 reads and 4,153 Mb of Illumina reads.

For all of the following programs, default parameters were used except where otherwise specified.

De novo assembly was performed using MIRA (version 4.0) (11). The draft genome has 137 contigs larger than 500 bp, which were assembled into 16 scaffolds, with a calculated total length of 5,613,242 bp (average depth of coverage, 30×), a G+C content of 59%, and an N_{50} contig size of 380,062 bp. The largest scaffold generated was 1,367,376 bp, and the N_{50} scaffold size was 559,889 bp. Genome-based taxonomy assigned strain PMB3(1) to the species *Collimonas pratensis* (digital DNA-DNA hybridization [dDDH] value, 84%; <https://tygs.dsmz.de>). The genome of PMB3(1) comprises a total of 5,136 predicted protein-coding genes and 52 tRNA genes.

Citation Picard L, Oger P, Turpault M-P, Uroz S. 2020. Draft genome sequence of *Collimonas pratensis* strain PMB3(1), an effective mineral-weathering and chitin-hydrolyzing bacterial strain. *Microbiol Resour Announc* 9:e00601-20. <https://doi.org/10.1128/MRA.00601-20>.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

Copyright © 2020 Picard et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Stéphane Uroz, stephane.uroz@inrae.fr.

Received 22 May 2020

Accepted 20 August 2020

Published 10 September 2020

According to RAST (12), 12% of the predicted proteins appeared involved in carbohydrate metabolism, including the Entner-Doudoroff pathway, in which glucose is oxidized to gluconate. The production of gluconate was proposed to play a role in mineral weathering (13). However, no pyrroquinoline quinone (PQQ) system was detected. Based on genome analysis, strain PMB3(1) may produce metabolites with antibacterial (rhizomide and feglymycin) or antifungal (iturin) activities as well as siderophores and organic acids. These activities suggest that PMB3(1) is well equipped to live in the rhizosphere of plants growing in nutrient-poor environments, to inhibit fungal growth, and to mobilize nutrients through its mineral-weathering potential, making it a promising growth-promoting and biocontrol agent (7, 14).

Data availability. The whole-genome and raw sequences are available under the accession no. [WXXL00000000](https://www.ncbi.nlm.nih.gov/nuclseq/WXXL00000000) and [SRX8380211](https://www.ncbi.nlm.nih.gov/nuclseq/SRX8380211) through [SRX8380213](https://www.ncbi.nlm.nih.gov/nuclseq/SRX8380213), respectively.

ACKNOWLEDGMENTS

This work was supported by grants from the EC2CO program of the CNRS to S.U. and P.O. and the Labex ARBRE (GeMM) project to S.U. L.P. was also supported by a fellowship from the French Ministère de l'Enseignement Supérieur, de la Recherche et de l'Innovation. The UMR 1136 and UR 1138 programs are supported by the ANR through the Laboratory of Excellence Arbre (ANR-11-LABX-0002-01).

We thank C. Calvaruso and P. Frey-Klett for harvesting and isolating the bacterial collection from Breuil-Chenue forest.

REFERENCES

1. Uroz S, Calvaruso C, Turpault MP, Sarniguet A, de Boer W, Leveau JHJ, Frey-Klett P. 2009. Efficient mineral weathering is a distinctive functional trait of the bacterial genus *Collimonas*. *Soil Biol Biochem* 41:2178–2186. <https://doi.org/10.1016/j.soilbio.2009.07.031>.
2. Koele N, Turpault M-P, Hildebrand EE, Uroz S, Frey-Klett P. 2009. Interactions between mycorrhizal fungi and mycorrhizosphere bacteria during mineral weathering: budget analysis and bacterial quantification. *Soil Biol Biochem* 41:1935–1942. <https://doi.org/10.1016/j.soilbio.2009.06.017>.
3. de Boer W, Leveau JHJ, Kowalchuk GA, Klein Gunnewiek PJA, Abeln ECA, Figge MJ, Sjollem K, Janse JD, van Veen JA. 2004. *Collimonas fungivorans* gen. nov., sp. nov., a chitinolytic soil bacterium with the ability to grow on living fungal hyphae. *Int J Syst Evol Microbiol* 54:857–864. <https://doi.org/10.1099/ijs.0.02920-0>.
4. Hoppener-Ogawa S, de Boer W, Leveau JHJ, van Veen JA, de Brandt E, Vanlaere E, Sutton H, Dare DJ, Vandamme P. 2008. *Collimonas arenae* sp. nov. and *Collimonas pratensis* sp. nov., isolated from (semi-)natural grassland soils. *Int J Syst Evol Microbiol* 58:414–419. <https://doi.org/10.1099/ijs.0.65375-0>.
5. Lee SD. 2018. *Collimonas antrihumi* sp. nov., isolated from a natural cave and emended description of the genus *Collimonas*. *Int J Syst Evol Microbiol* 68:2448–2453. <https://doi.org/10.1099/ijs.0.002855>.
6. Leveau JHJ, Uroz S, de Boer W. 2010. The bacterial genus *Collimonas*: mycophagy, weathering and other adaptive solutions to life in oligotrophic soil environments. *Environ Microbiol* 12:281–292. <https://doi.org/10.1111/j.1462-2920.2009.02010.x>.
7. Doan HK, Maharaj NN, Kelly KN, Miyao EM, Davis RM, Leveau JHJ. 2019. Antimycotal activity of *Collimonas* isolates and synergy-based biological control of fusarium wilt of tomato. *Phytobiomes J* 4:64–74. <https://doi.org/10.1094/PBIOMES-05-19-0027-R>.
8. Uroz S, Calvaruso C, Turpault MP, Pierrat JC, Mustin C, Frey-Klett P. 2007. Effect of the mycorrhizosphere on the genotypic and metabolic diversity of the bacterial communities involved in mineral weathering in a forest soil. *Appl Environ Microbiol* 73:3019–3027. <https://doi.org/10.1128/AEM.00121-07>.
9. Calvaruso C, Turpault M-P, Leclerc E, Frey-Klett P. 2007. Impact of ectomycorrhizosphere on the functional diversity of soil bacterial and fungal communities from a forest stand in relation to nutrient mobilization processes. *Microb Ecol* 54:567–577. <https://doi.org/10.1007/s00248-007-9260-z>.
10. Pospiech A, Neumann B. 1995. A versatile quick-prep of genomic DNA from Gram-positive bacteria. *Trends Genet* 11:217–218. [https://doi.org/10.1016/s0168-9525\(00\)89052-6](https://doi.org/10.1016/s0168-9525(00)89052-6).
11. Chevreux B, Wetter T, Suhai S. 1999. Genome sequence assembly using trace signals and additional sequence information, p 45–56. *In* Computer science and biology: proceedings of the German Conference on Bioinformatics, GCB '99. GCB, Hannover, Germany.
12. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
13. Babu-Khan S, Yeo TC, Martin WL, Duron MR, Rogers RD, Goldstein AH. 1995. Cloning of a mineral phosphate-solubilizing gene from *Pseudomonas cepacia*. *Appl Environ Microbiol* 61:972–978. <https://doi.org/10.1128/AEM.61.3.972-978.1995>.
14. Shinohara H, Hirose Y. 4 February 2016. Novel *Collimonas* bacteria and method for controlling harmful plant pathogen using said bacteria. US patent application 14/774,012.